

GAATTCGGGCACGAGGCGGGTTGCAGTATGAGTCGCCAATCGGACCTAGTGAGGAGCTTCTTGGAGCAGCAGGAG	75
M S R Q S D L V R S F L E Q Q E	16
CCCCGGGACCACCGGAAGGGGCAATCCTCGCCGTGAGTTACAGCGACATTAAAGCCCGCTCAGTGGGTTGGAAG	150
A R D H R K G A I L A R E F S D I K A R S V A W K	41
ACTGAAGTGTGTGCTCCACTAAAGCCGGCAGTCAGCAGGGAAGCTCAAAGAAGAACCGCTACAAAGACGTGGTA	225
T E G V C S T K A G S Q Q G N S K K N R Y K D V V	66
CCGTATGATGAGACGAGAGTCATCCTTTCCCTGCTCCAGGAGGAAGGACACGGAGATTACATTAATGCCAACTTC	300
P Y D E T R V I L L Q E E G H G D Y I N A N F	91
ATCCGGGGCACAGATGGAAGCCAGGCTACATTGCGACGCAAGGACCCCTGCCTCACACTCTGTTGGACTTCTGG	375
I R G T D G S Q A Y I A T Q G P L P H T L L D F W	116
CGCCTGGTTGGGAGTTTGGAAATCAAGGTGATCTTGATGGCCTGTGAGGACAGAAAATGGACGGAGGAAGTGT	450
R L V W E F G I K V I L M A C Q G E T E N G R R K C	141
GAACGCTACTGGGCCCAGGAGCGGGAGCCTCTACAGGCCGGGCTTCTGTCATCACCTTGACAAAGGAGACAGCA	525
E R Y W A Q E R E P L Q A G P F C I T L T K E T A	166
CTGACTTCGGACATCACTCTCAGGACCCCTCCAGGTTACATTCCAGAAGGAATCCCGTCTGTGCACCAGCTACAG	600
L T S D I T L R T L Q V T F Q K E S R P V H Q L Q	191
TACATGTCTTGGCCGGACACGGGGTCCCAGCAGTTCCGATCACATTCTCACCATGGTGAGGAGGCCGTTGC	675
Y M S W P D H G V P S S S D H I L T M V E E A R C	216
CTCCAAGGACTTGGACCTGGACCCCTCTGTGTCCACTGCAGTGTCTGGCTGTGGACGAACAGGTGTCTTGTGTGCT	750
L Q G L G P G P L C V H C S A G C G R T G V L C A	241
GTTGATTACGTGAGGCAGTTGCTTCTGACTCAGACAATCCCAACCAATTTAGCCTCTTTGAAGTGGTCTGGAG	825
V D Y V R Q L L L T Q T I P P N F S L F E V - V L E	266
ATGCGGAAACAGCGACCTGCAGCGGTGCAGACAGAGGAGCAGTACAGGTTCCCTGTACCACACAGTGGCTCAGCTA	900
M R K Q R P A A V Q T E E Q Y R F L Y H T V A Q L	291
TTCTCCGCACTCTCCAGAACAACAGTCCCCTCTACCAGAACCTCAAGGAGAACCGCGCTCCAATCTGCAAGGAC	975
F S R T L Q N N S P L Y Q N L K E N R A P I C K D	316
TCCTCGTCCCTCAGGACTCTCAGCCCTGCTGCCACATCCCGCCCACTGGGTGGCGTTCTCAGGACATCTCG	1050
S S S L R T S S A L P A T S R P L G G V L R S I S	341
GTGCTGGGCCACCGACCTTCCCATGGCTGACACTTACGCTGTGGTGAGAAGCGTGGCGCTTCCGGCAGCACA	1125
V P G P P T L P M A D T Y A V V Q K R G A S G S T	366
GGGCCGGGCACGCGGGCGCCCAACAGCACGGACACCCGATCTACAGCCAGGTGGCTCCACGTATCCAGCGGCC	1200
G P G T R A P N S T D T P I Y S Q V A P R I Q R P	391
GTGTACACACCGAAAACGCGCAGGGGACAACGGCACTGGGCGGAGTTTCTGCGGATGAAAACCTTCCGGGCT	1275
V S H T E N A Q G T T A L G R V P A D E N P S G P	416
GATGCTATGAGGAAGTAACAGATGGAGCGCAGACTGGTGGGCTAGGCTTCAACTTGCGCATTGGAAGACCTAAA	1350
D A Y E E V T D G A Q T G G L G F N L R I G R P K	441
GGGCCAGGGATCTCCAGCGGAGTGGACACGGGTGTAATGAGTGCTGTACCAGTTCCAGCCTGTCACTCAGTGG	1425
G G P R D P P A E W T R V *	453
TGGCTGGGCGACTGCAACCCCATGCTGCTGTGTGCTGCTTATGTATGAGTGGGACTCATGGGCTGAATCAAA	1500
ATAAAAGTTTCTCAGGGTAGAAAAAACAATAGGCACTTGGCCAGTGGTTATAGCAGTCAAAGCCAGGGGCTA	1575
GGAGGGGTAGTGGGGAGGTGGTGGATCTACTCTAGAGAAAGTTTAGGAAGCACATCAAGAGTGAGCATGCCA	1650
CTCTTCTCCCATCACTACTGGAAGGTGCACCCAGACAGAGTCTTAAGTACCTCATGTAACTTGCAATGAGC	1725
GCTACCTGGATGGACATGTCTGGCCCTACAGCTAGAGACATGTCTAATTAGATCTCATGTAACTTGCAATGAGC	1800
TAGAAAGATCTCCGTCTGGTTCAGGAAATGGATCACTACCTAGTCAGGTAATAGTGTGCCATCCAGAAGACGAAT	1875
GCAAGTACCGTCTTCTCAAAATGGAAGAAAATAGATCCTCAAGAAATAATGTATGTACAACTGTCTACGCCCT	1950
CTGACTGCCCTGCCCTCACTGCCATAATGTCAAAACAAGTCAGGCTTATATGACAGTTGTTTCATCTAGTCAGTC	2025
CTTCTACCGGAACTGTAAACATCATTAAATTTAATGTAGAATTCAATAAGAGTGGGTCAAAAACCTCAA	2100
AAAAAAGAGTGGGTCAAAAACCTCAA	2175
AAAAAAGAGTGGGTCAAAAACCTCAA	2226

[illegible]

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MCLK1	MRHSKRTYC-----PDWDERDWDYGTWRSSSSHKRKRSHSSAREOKR	43
MCLK2	P.PR.YHSSERGRSGSYHEHYQSRKHKRRR.R.WSSSSDRTRRR.REDS	50
MCLK3	H.C..YRSPEPDPYLTYRWK.RRS.SREHEGLRYPSR.EPPPR.S---	47
MCLK4H.-----S.ESWGHEGY.G-.....R.....TO.NRH	42
MCLK1	CRYDHSKTTDSYILESRSINEKAYHSRRYVDEY--RNDYMGYEPGHPYGE	91
MCLK2	YHVRSSRSY.DHSSDR.LY-----D.RYCGSYR....SRDRGEAY.DT	93
MCLK3	SRE.APYRTRKHAHHCHK.RTRSCSSASSRSQQSSKRSSR-----	94
MCLK4	KPH.QFKDSDCHYLEARCLNERDYRD.RYIDEY-....CEGYVPRH.HR	91
MCLK1	PGSRYQMHS-SKSSGRSGRSSYKSKHRSRHHTSQHHS DGHSHRRKRSRSV	140
MCLK2	DFRQSYEYHREN..Y..Q...RRKHR.R.RRSRTFSRSSSHSS.RAK-..	142
MCLK3	SRE.APYRTRKHAHHCHK.RTRSCSSASSRSQQSSKRSSR-----	136
MCLK4	DVESTYRIHC....V..R...P.R.RNRPCASH.S-----I	139
MCLK1	EDDEEGHLICQSGDVLSARYEIVDTLGEAFGKVVECIDHKVGRRVAVK	190
MCLK2	...A.....YHV..W.QE.....S.....TS.R..Q...RR..T...L.	192
MCLK3	...K...V.RI.SW.QE.....GN...T.....L..ARGKSQ..L.	186
MCLK4R.....GMD.LH....	189
MCLK1	IVKNVDRYCEAAQSEIQVLEHLNTTDPHSTFRCVQMLEWFEHRGHICIVF	240
MCLK2	.I...EK.K...RL..N...KI.EK..KNKNL....FD..DYH..M..S.	242
MCLK3	.IR..GH.R...RL..N..KKIKEK.KENK.L..L.SD.NFH..M..A.	236
MCLK4	...GG.R...R.....S...N.V.....D.H..V....	239
MCLK1	ELLGLSTYDFIKENSFLPFRMDHIRKMAYQICKSVNFLHSNKLTHTDLKP	290
MCLK2F..L.D.NY..YPIHQV.H..F.L.QA.K...D.....	292
MCLK3	...KN.FE.L...N.Q.YPLP.V.H...L.HALR...E.Q.....	286
MCLK4QI...Q.....Q.I...H.....	289
MCLK1	ENILFVKSDYTEANPKMKRDERTIVNPDIKVVDGFSATYDDEHHSTLVS	340
MCLK2N...ELT..LEK.....SVKSTAVR.....F.H....I..	342
MCLK3N..EFETL..EHKSCE.KSVK.TSIR.A.....F.H...T.I.A	336
MCLK4VVK..S.....LK.T.....****	339
MCLK1	TRHYRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFPTHDSREHLAMM	390
MCLK2E.....IF...V...L.Q...N.....	392
MCLK3P.....E...A.....F...R...L.Q...K.....	386
MCLK4Q...K.....	389
MCLK1	ERILGPLPKHMIQKTRKRRYFHHDRLDWDEHSSAGRYVSRCKPLKEFML	440
MCLK2V.SR..R...QK..YRG.....NT.....REN....RRYLT	442
MCLK3	.K...I.S...HR...QK..YKGG.V...N..D...KEN....SY..	436
MCLK4I.A.....K...NQ.....R.....	439
MCLK1	SQDAEHEFLFDLVGKILEYDPAKRITLKEALKHPFFYPLKKHT	483
MCLK2	.EAED.HQ....IENM...E....L..G...Q....AC.RTEPPNTKLWD	492
MCLK4	QDSL..VQ....MRRM..F...Q...A...L....AG.TPEERSFHSSSR	486
MCLK5	CHDE...K....RRM.....R...D...Q....DL..RK	489
MCLK1	SSRDISR	499
MCLK2	NPSR	496
MCLK3		
MCLK4		

FIGURE 4

SIRP4
SIRP1

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	MEPAGPAPGRIGPLLCLLLAASCAWSGVAGEEELQVIQPEKSVSVAAGESAIIHCTVT	58
	MPVPASWPHIPSPFLIMTLLLGRLTGVAGEEELQVIQPEKSVSVAAGESAIIHCTVT	57
4	SLIPVGPIQWFRGAGPARELIYNQKEGHFPRVTTVSESTKRENNDFSISISNITPADA	116
1	SLIPVGPIQWFRGAGAGRELIYNQKEGHFPRVTTVSESTKRENNDFSISISNITPADA	115
4	GTYCYVKFRKGSPT-EFKSGAGTELSVRAKPSAPVVSQPAARATECHTVSFTCESHG	173
1	GTYCYVKFRKGSPTDOVEFKSGAGTELSVRAKPSAPVVSQPAARATECHTVSFTCESHG	173
4	FSPRDITLKWFKNGNELSDFQTNVDVGEVSYSIHSTAKVVLTREDVHSQVICEVAH	231
1	FSPRDITLKWFKNGNELSDFQTNVDVGEVSYSIHSTAKVVLTREDVHSQVICEVAH	231
4	VTLQGDPLRG TANLSEAIRVPPTLEVTOQHVR AENQNVTCQVRKFYFQRLQLTWLEN	289
1	ITLQGDPLRG TANLSEAIRVPPTLEVTOQHVR AENQNVTCQVSNFYERGLQLTWLEN	289
4	GNVSRTETASTVTENKDGTYNWM SWLLVNVSAHRDDVLTLCQVEHDGQPAVSKSHDLK	347
1	GNVSRTETASTVTENKDGTYNWM SWLLVNVSAHRDDVLTLCQVEHDGQPAVSKSYALE	347
4	VSAHPKEGGSNTAAENTGSNERNIYIVVG VVCTLLVALLMAALYLVRIRQKKAQGSTS	405
1	ISAHQKEHGSNTAAENTGSNERNIYIVVG VVCTLLVALLMAALYLVRIRQKKAQGSTS	398
4	STRLHEPEKNAREITQDTNDITYADLNLPKGKKPAPQAAEPNNHTEYASIQTSPPAS	463
4	EDTLTYADLDMVHLNRTPKQPAPKPEPSFSEYASVQVPRK	503

Figure 5